

AMENDMENTS

1. (Currently amended) A method for identifying a polypeptide, comprising:

(a) determining two or more characteristics ~~at least a first and second characteristic~~ associated with said polypeptide, or a peptide fragment thereof, one of said characteristics ~~said first characteristic~~ being mass of a peptide fragment of said polypeptide determined by mass spectrometry;

(b) comparing said characteristics associated with said polypeptide to an annotated polypeptide index, said annotated polypeptide index comprising at least one empirically determined characteristic for each of the polypeptides in the index~~], with the proviso that said annotated polypeptide index is not a sequence database, wherein said empirically determined characteristic is determined as for said second characteristic in step (a)]~~; and

(c) identifying one or more polypeptides in said annotated polypeptide index having said characteristics.

2. (Original) The method of claim 1, further comprising:

(d) determining one or more additional characteristics associated with said polypeptide;

(e) comparing said characteristics determined in step (a) and step (d) to said annotated polypeptide index; and

(f) optionally repeating steps (d) and (e) one or more times, wherein a set of characteristics is determined that identifies a single polypeptide in said annotated polypeptide index.

3. (Original) The method of claim 1, further comprising quantitating the amount of said identified polypeptide in a sample containing said polypeptide.

4. (Original) The method of claim 1, wherein said fragment mass is determined at an accuracy in part per million of 1 ppm or greater ppm.

5. (Original) The method of claim 1, wherein said fragment mass is determined at an accuracy in ppm of 2.5 ppm or greater ppm.

6. (Original) The method of claim 1, wherein said fragment mass is determined at an accuracy in ppm of 5 ppm or greater ppm.

7. (Original) The method of claim 1, wherein said fragment mass is determined at an accuracy in ppm of 10 ppm or greater ppm.

8. (Original) The method of claim 1, wherein said fragment mass is determined at an accuracy in ppm of 100 ppm or greater ppm.

9. (Original) The method of claim 1, wherein three or more characteristics of said polypeptide are determined.

10. (Original) The method of claim 1, wherein four or more characteristics of said polypeptide are determined.

11. (Original) The method of claim 1, wherein five or more characteristics of said polypeptide are determined.

12. (Original) The method of claim 1, wherein said characteristics are selected from the group consisting of polypeptide mass, amino acid composition, pI, and order of elution on a chromatographic medium.

13. (Currently amended) A method for identifying and quantitating a polypeptide, comprising:

(a) determining two or more characteristics ~~at least a first and second characteristic~~ associated with a polypeptide in a sample, or a peptide fragment thereof, ~~said first characteristic~~ one of said characteristics being mass of a peptide fragment of said polypeptide determined by mass spectrometry;

(b) comparing said characteristics associated with said polypeptide to an annotated polypeptide index, said annotated polypeptide index comprising at least one empirically determined characteristic for each of the polypeptides in the index, ~~with the proviso that said annotated polypeptide index is not a sequence database, wherein said empirically determined characteristic is determined as for said second characteristic in step (a);~~

(c) identifying one or more polypeptides in said annotated polypeptide index having said characteristics; and

(d) quantitating the amount of said identified polypeptide in said sample containing said polypeptide by comparison to a standard corresponding to said polypeptide, or said peptide fragment thereof.

14. (Original) The method of claim 13, further comprising

(e) determining one or more additional characteristics associated with said polypeptide; and

(f) comparing said characteristics determined in step (a) and step (e) to said annotated polypeptide index; and

(g) optionally repeating steps (e) and (f) one or more times, wherein a set of characteristics is determined that identifies a single polypeptide in said annotated polypeptide index.

15. (Original) The method of claim 13, wherein said fragment mass is determined at an accuracy in ppm of 1 ppm or greater ppm.

16. (Original) The method of claim 13, wherein said fragment mass is determined at an accuracy in ppm of 2.5 ppm or greater ppm.

17. (Original) The method of claim 13, wherein said fragment mass is determined at an accuracy in ppm of 5 ppm or greater ppm.

18. (Original) The method of claim 13, wherein said fragment mass is determined at an accuracy in ppm of 10 ppm or greater ppm.

19. (Original) The method of claim 13, wherein said fragment mass is determined at an accuracy in ppm of 100 ppm or greater ppm.

20. (Original) The method of claim 13, wherein three or more characteristics of said polypeptide are determined.

21. (Original) The method of claim 13, wherein four or more characteristics of said polypeptide are determined.

22. (Original) The method of claim 13, wherein five or more characteristics of said polypeptide are determined.

23. (Original) The method of claim 13, wherein said characteristics are selected from the group consisting of polypeptide mass, amino acid composition, pI, and order of elution on a chromatographic medium.

24. (Withdrawn) A method for generating a polypeptide identification index, comprising:

(a) determining a set of two or more characteristics associated with a first polypeptide, or a fragment thereof, one of said characteristics being the mass of a fragment of said polypeptide, said fragment mass being determined by mass spectrometry;

(b) repeating step (a) for a second polypeptide;

(c) optionally determining one or more additional characteristics associated with said first and second polypeptides, wherein said determined characteristics are sufficient to distinguish said first and second polypeptides, thereby generating a polypeptide identification index for said first and second polypeptides.

25. (Withdrawn) The method of claim 24, further comprising repeating steps (a) through (c) one or more times for a different polypeptide, wherein said determined characteristics are sufficient to distinguish each of said polypeptides, thereby generating a polypeptide identification index for each of said polypeptides.

26. (Withdrawn) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 1 ppm or greater ppm.

27. (Withdrawn) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 2.5 ppm or greater ppm.

28. (Withdrawn) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 5 ppm or greater ppm.

29. (Withdrawn) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 10 ppm or greater ppm.

30. (Withdrawn) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 100 ppm or greater ppm.

31. (Withdrawn) The method of claim 24, wherein said characteristics are selected from the group consisting of polypeptide mass, amino acid composition, pI, and order of elution on a chromatographic medium.

32. (Withdrawn) A method of identifying a polypeptide, comprising:

(a) determining a set of characteristics associated with said polypeptide, or a fragment thereof, one of said characteristics being the mass of a fragment of said polypeptide, said fragment mass being determined by mass spectrometry;

(b) comparing said determined characteristics to a polypeptide identification index generated by the method of claim 24; and (c) identifying one or more polypeptides of said polypeptide identification index having said set of characteristics.

33. (Withdrawn) The method of claim 32, further comprising:

(d) determining one or more additional characteristics associated with said polypeptide;

(e) comparing said characteristics determined in step (a) and step (d) to said polypeptide identification index; and

(f) optionally repeating steps (d) and (e) one or more times, wherein a set of characteristics is determined that identifies a single polypeptide in said polypeptide identification index.

34. (Withdrawn) The method of claim 32, further comprising quantitating the amount of said identified polypeptide in a sample containing said polypeptide.

35. (Withdrawn) The method of claim 32, wherein said fragment mass is determined at an accuracy in ppm of 1 ppm or greater ppm.

36. (Withdrawn) The method of claim 32, wherein said fragment mass is determined at an accuracy in ppm of 2.5 ppm or greater ppm.

37. (Withdrawn) The method of claim 32, wherein said fragment mass is determined at an accuracy in ppm of 5 ppm or greater ppm.

38. (Withdrawn) The method of claim 32, wherein said fragment mass is determined at an accuracy in ppm of 10 ppm or greater ppm.

39. (Withdrawn) The method of claim 32, wherein said fragment mass is determined at an accuracy in ppm of 100 ppm or greater ppm.

40. (Withdrawn) The method of claim 32, wherein three or more characteristics of said polypeptide are determined.

41. (Withdrawn) The method of claim 32, wherein four or more characteristics of said polypeptide are determined.

42. (Withdrawn) The method of claim 32, wherein five or more characteristics of said polypeptide are determined.

43. (Withdrawn) The method of claim 32, wherein said characteristics are selected from the group consisting of polypeptide mass, amino acid composition, pI, and order of elution on a chromatographic medium.

44. (Previously entered) The method of claim 1, wherein at least one of said characteristics is determined by chromatography.

45. (Previously entered) The method of claim 44, wherein at least one of said characteristics is determined by ion exchange chromatography.

46. (Previously entered) The method of claim 45, wherein at least one of said characteristics is determined by anion exchange chromatography.

47. (Previously entered) The method of claim 45, wherein at least one of said characteristics is determined by cation exchange chromatography.

48. (Previously entered) The method of claim 44, wherein at least one of said characteristics is determined by gel filtration chromatography.

49. (Previously entered) The method of claim 44, wherein at least one of said characteristics is determined by reverse phase chromatography.

50. (Previously entered) The method of claim 1, wherein at least one of said characteristics is determined by electrophoresis.

51. (Previously entered) The method of claim 13, wherein said standard is added to said sample.

52. (Previously entered) The method of claim 13, wherein said standard is a differentially isotopically labeled version of the polypeptide being quantitated.